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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/837,992

DATE: 10/11/2001

TIME: 09:29:54

Input Set : A:\-60-2.app

Output Set: N:\CRF3\10112001\I837992.raw

3 <110> APPLICANT: Tian, Hui
 4 Schultz, Joshua
 5 Shan, Bei
 6 Tularik Inc.
 8 <120> TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG): Compositions
 9 and Methods of Use
 11 <130> FILE REFERENCE: 018781-006020US
 13 <140> CURRENT APPLICATION NUMBER: US 09/837,992
 14 <141> CURRENT FILING DATE: 2001-04-18
 16 <150> PRIOR APPLICATION NUMBER: US 60/198,465
 17 <151> PRIOR FILING DATE: 2000-04-18
 19 <150> PRIOR APPLICATION NUMBER: US 60/204,234
 20 <151> PRIOR FILING DATE: 2000-05-15
 22 <160> NUMBER OF SEQ ID NOS: 45
 24 <170> SOFTWARE: PatentIn Ver. 2.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 652
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Mus musculus
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: mouse sitosterolemia susceptibility gene (SSG)
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 40 20 25 30
 42 Thr Glu Ala Arg His Ser Leu Gly Val Leu His Val Ser Tyr Ser Val
 43 35 40 45
 45 Ser Asn Arg Val Gly Pro Trp Trp Asn Ile Lys Ser Cys Gln Gln Lys
 46 50 55 60
 48 Trp Asp Arg Gln Ile Leu Lys Asp Val Ser Leu Tyr Ile Glu Ser Gly
 49 65 70 75 80
 51 Gln Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu
 52 85 90 95
 54 Leu Asp Ala Ile Ser Gly Arg Leu Arg Arg Thr Gly Thr Leu Glu Gly
 55 100 105 110
 57 Glu Val Phe Val Asn Gly Cys Glu Leu Arg Arg Asp Gln Phe Gln Asp
 58 115 120 125
 60 Cys Phe Ser Tyr Val Leu Gln Ser Asp Val Phe Leu Ser Ser Leu Thr
 61 130 135 140
 63 Val Arg Glu Thr Leu Arg Tyr Thr Ala Met Leu Ala Leu Cys Arg Ser
 64 145 150 155 160
 66 Ser Ala Asp Phe Tyr Asn Lys Lys Val Glu Ala Val Met Thr Glu Leu
 67 165 170 175
 69 Ser Leu Ser His Val Ala Asp Gln Met Ile Gly Ser Tyr Asn Phe Gly
 70 180 185 190

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75 Leu Gln Asp Pro Lys Val Met Met Leu Asp Glu Pro Thr Thr Gly Leu
76      210                        215                220
78 Asp Cys Met Thr Ala Asn Gln Ile Val Leu Leu Leu Ala Glu Leu Ala
79 225                        230                235                240
81 Arg Arg Asp Arg Ile Val Ile Val Thr Ile His Gln Pro Arg Ser Glu
82      245                        250                255
84 Leu Phe Gln His Phe Asp Lys Ile Ala Ile Leu Thr Tyr Gly Glu Leu
85      260                        265                270
87 Val Phe Cys Gly Thr Pro Glu Glu Met Leu Gly Phe Phe Asn Asn Cys
88      275                        280                285
90 Gly Tyr Pro Cys Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp
91      290                        295                300
93 Leu Thr Ser Val Asp Thr Gln Ser Arg Glu Arg Glu Ile Glu Thr Tyr
94 305                        310                315                320
96 Lys Arg Val Gln Met Leu Glu Cys Ala Phe Lys Glu Ser Asp Ile Tyr
97      325                        330                335
99 His Lys Ile Leu Glu Asn Ile Glu Arg Ala Arg Tyr Leu Lys Thr Leu
100      340                        345                350
102 Pro Met Val Pro Phe Lys Thr Lys Asp Pro Pro Gly Met Phe Gly Lys
103      355                        360                365
105 Leu Gly Val Leu Leu Arg Arg Val Thr Arg Asn Leu Met Arg Asn Lys
106      370                        375                380
108 Gln Ala Val Ile Met Arg Leu Val Gln Asn Leu Ile Met Gly Leu Phe
109 385                        390                395                400
111 Leu Ile Phe Tyr Leu Leu Arg Val Gln Asn Asn Thr Leu Lys Gly Ala
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117 Tyr Thr Gly Met Leu Asn Ala Val Asn Leu Phe Pro Met Leu Arg Ala
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120 Val Ser Asp Gln Glu Ser Gln Asp Gly Leu Tyr His Lys Trp Gln Met
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123 Leu Leu Ala Tyr Val Leu His Val Leu Pro Phe Ser Val Ile Ala Thr
124 465                        470                475                480
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138 Ile Gly Ser Gly Phe Ile Arg Asn Ile Gln Glu Met Pro Ile Pro Leu
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147 Thr Ser Met Leu Asn His Pro Met Cys Ala Ile Thr Gln Gly Val Gln
148          595          600          605
150 Phe Ile Glu Lys Thr Cys Pro Gly Ala Thr Ser Arg Phe Thr Ala Asn
151          610          615          620
153 Phe Leu Ile Leu Tyr Gly Phe Ile Pro Ala Leu Val Ile Leu Gly Ile
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170 <222> LOCATION: (47)..(2005)
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177 ggagcaaggt tcggtcacgg gcacagaggg tcggcacagc ttaggtgtcc tgcattgtgc 180
178 ctacagcgtc agcaaccgtg tcgggccttg gtggaacatc aaatcatgcc agcagaagtg 240
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183 gcgcgagacg ttgcgataca cagcgatgct ggccctctgc cgcagctccg cggacttcta 540
184 caacaagaag gttagaggcag tcatgacaga gctgagcctg agccacgtgg cggaccaaatt 600
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189 catcctgact tacggagagt tgggtgttct tggcacccca gaggagatgc ttggcttctt 900
190 caataactgt ggttaccctt gtctgaaca ttccaatccc tttgattttt acatggactt 960
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192 gctggaatgt gccttcaagg aatctgacat ctatcacaaa attctggaga acattgaaag 1080
193 agcacgatac ctgaaaacct taccatgggt tcttttcaaa acaaaagatc ctctgggat 1140
194 gttcggcaag cttggtgtcc tgctgaggcg agtaacaaga aacttaatga ggaataagca 1200
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199 gctcgccctac gtgctacacg tctctccctt cagcgtcatc gccacgggtc ttttcagcag 1500
200 tgtgtgttat tggactctgg gcttgatatc tgaagttgcc agatttgat atttctctgc 1560
201 tgctcttttg gccctcact taattggaga atttctaaca cttgtgctgc ttggtatagt 1620
202 ccaaaaccct aatattgtca acagtatagt ggctctgctc agcatctctg ggctgcttat 1680

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205 cttcacttgt ggtggatcca acacctctat gctaaatcac ccgatgtgcg ccatcaccca 1860
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210 ccttgtgtct gacccttgtg tctatccgga gcccgaagg caacgagAAC tcacagccct 2160
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228 Val Asn Arg Gly Ser Gln Ser Ser Leu Glu Gly Ala Pro Ala Thr Ala
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231 Pro Glu Pro His Ser Leu Gly Ile Leu His Ala Ser Tyr Ser Val Ser
232 35 40 45
234 His Arg Val Arg Pro Trp Trp Asp Ile Thr Ser Cys Arg Gln Gln Trp
235 50 55 60
237 Thr Arg Gln Ile Leu Lys Asp Val Ser Leu Tyr Val Glu Ser Gly Gln
238 65 70 75 80
240 Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu Leu
241 85 90 95
243 Asp Ala Met Ser Gly Arg Leu Gly Arg Ala Gly Thr Phe Leu Gly Glu
244 100 105 110
246 Val Tyr Val Asn Gly Arg Ala Leu Arg Arg Glu Gln Phe Gln Asp Cys
247 115 120 125
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253 145 150 155 160
255 Pro Gly Ser Phe Gln Lys Lys Val Glu Ala Val Met Ala Glu Leu Ser
256 165 170 175
258 Leu Ser His Val Ala Asp Arg Leu Ile Gly Asn Tyr Ser Leu Gly Gly
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262 195 200 205
264 Gln Asp Pro Lys Val Met Leu Phe Asp Glu Pro Thr Thr Gly Leu Asp
265 210 215 220
267 Cys Met Thr Ala Asn Gln Ile Val Val Leu Leu Val Glu Leu Ala Arg
268 225 230 235 240
270 Arg Asn Arg Ile Val Val Leu Thr Ile His Gln Pro Arg Ser Glu Leu

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271                245                250                255
273 Phe Gln Leu Phe Asp Lys Ile Ala Ile Leu Ser Phe Gly Glu Leu Ile
274                260                265                270
276 Phe Cys Gly Thr Pro Ala Glu Met Leu Asp Phe Phe Asn Asp Cys Gly
277                275                280                285
279 Tyr Pro Cys Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp Leu
280                290                295                300
282 Thr Ser Val Asp Thr Gln Ser Lys Glu Arg Glu Ile Glu Thr Ser Lys
283 305                310                315                320
285 Arg Val Gln Met Ile Glu Ser Ala Tyr Lys Lys Ser Ala Ile Cys His
286                325                330                335
288 Lys Thr Leu Lys Asn Ile Glu Arg Met Lys His Leu Lys Thr Leu Pro
289                340                345                350
291 Met Val Pro Phe Lys Thr Lys Asp Ser Pro Gly Val Phe Ser Lys Leu
292                355                360                365
294 Gly Val Leu Leu Arg Arg Val Thr Arg Asn Leu Val Arg Asn Lys Leu
295                370                375                380
297 Ala Val Ile Thr Arg Leu Leu Gln Asn Leu Ile Met Gly Leu Phe Leu
298 385                390                395                400
300 Leu Phe Phe Val Leu Arg Val Arg Ser Asn Val Leu Lys Gly Ala Ile
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309 Ser Asp Gln Glu Ser Gln Asp Gly Leu Tyr Gln Lys Trp Gln Met Met
310                450                455                460
312 Leu Ala Tyr Ala Leu His Val Leu Pro Phe Ser Val Val Ala Thr Met
313 465                470                475                480
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316                485                490                495
318 Ala Arg Phe Gly Tyr Phe Ser Ala Ala Leu Leu Ala Pro His Leu Ile
319                500                505                510
321 Gly Glu Phe Leu Thr Leu Val Leu Leu Gly Ile Val Gln Asn Pro Asn
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331                565                570                575
333 Val Asn Glu Phe Tyr Gly Leu Asn Phe Thr Cys Gly Ser Ser Asn Val
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336 Ser Val Thr Thr Asn Pro Met Cys Ala Phe Thr Gln Gly Ile Gln Phe
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340                610                615                620
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VERIFICATION SUMMARY

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